

METHODS AND COMPOSITIONS FOR
EFFICIENT NUCLEIC ACID SEQUENCING

ABSTRACT

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Disclosed are novel methods and compositions for
rapid and highly efficient nucleic acid sequencing based
upon hybridization with two sets of small oligonucleotide
probes of known sequences. Extremely large nucleic acid
10 molecules, including chromosomes and non-amplified RNA,
may be sequenced without prior cloning or subcloning
steps. The methods of the invention also solve various
current problems associated with sequencing technology
such as, for example, high noise to signal ratios and
15 difficult discrimination, attaching many nucleic acid
fragments to a surface, preparing many, longer or more
complex probes and labelling more species.

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